



SEQUENCE LISTING

BENAROUS, Richard
MARGOTTIN, Florence
DURAND, Hervé
ARENZANA SEISDEDOS, Fernando
KROLL, Mathias
CONDORCET, Jean-Paul

<120> Human beta-TrCP protein

<130> 935.38812X00

<140> US/09/601,168

<141> 2000-07-28

<150> PCT/FR99/00196

<151> 1999-01-29

<150> FR98 01100

<151> 1998-01-30

<150> FR98 15545

<151> 1998-12-09

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 2151

<212> DNA

<213> Artificial sequence

<220>

<221> CDS

<222> (70)..(1776)

<220>

<223> Description of the artificial sequence : cDNA
coding for human beta-TrCP protein

<400> 1

tgcgttggt gcggcctggc accaaagggg cggcccccggc ggagagcggg cccagtggcc 60
tcggcgatt atg gac ccg gcc gag gcg ctg ctg caa gag aag gca ctc aag 111
Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys
1 5 10
ttt atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct 159
Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro
15 20 25 30
agg aag ata ata cca gag aag aat tca ctt aga cag aca tac aac agc 207
Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser
35 40 45
tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act 255
Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr
50 55 60
gct atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc 303
Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly
65 70 75
act tcc agt atg att gtg ccc aag caa cgg aaa ctc tca gca agc tat 351
Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr
80 85 90
gaa aag gaa aag gaa ctg tgt gtc aaa tac ttt gag cag tgg tca gag 399
Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu
95 100 105 110

tca gat caa gtg gaa ttt gtg gaa cat ctt ata tcc caa atg tgt cat	447
Ser Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His	
115 120 125	
tac caa cat ggg cac ata aac tgc tat ctt aaa cct atg ttg cag aga	495
Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg	
130 135 140	
gat ttc ata act gct ctg cca gct cgg gga ttg gat cat atc gct gag	543
Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu	
145 150 155	
aac att ctg tca tac ctg gat gcc aaa tca cta tgt gct gct gaa ctt	591
Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu	
160 165 170	
gtg tgc aag gaa tgg tac cga gtg acc tct gat ggc atg ctg tgg aag	639
Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys	
175 180 185 190	
aag ctt atc gag aga atg gtc agg aca gat tct ctg tgg aga ggc ctg	687
Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu	
195 200 205	
gca gaa cga aga gga tgg gga cag tat tta ttc aaa aac aaa cct cct	735
Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro	
210 215 220	
gac ggg aat gct cct ccc aac tct tct tat aga gca ctt tat cct aaa	783
Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys	
225 230 235	
att ata caa gac att gag aca ata gaa tct aat tgg aga tgt gga aga	831
Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg	
240 245 250	
cat agt tta cag aga att cac tgc cga agt gaa aca agc aaa gga gtt	879
His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val	
255 260 265 270	
tac tgt tta cag tat gat gat cag aaa ata gta agc ggc ctt cga gac	927
Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp	
275 280 285	
aac aca atc aag atc tgg gat aaa aac aca ttg gaa tgc aag cga att	975
Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile	
290 295 300	
ctc aca ggc cat aca ggt tca gtc ctc tgt ctc cag tat gat gag aga	1023
Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg	
305 310 315	
gtg atc ata aca gga tca tgc gat tcc acg gtc aga gtg tgg gat gta	1071
Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val	
320 325 330	
aat aca ggt gaa atg cta aac acg ttg att cac cat tgt gaa gca gtt	1119
Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val	
335 340 345 350	
ctg cac ttg cgt ttc aat aat ggc atg atg gtg acc tgc tcc aaa gat	1167
Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp	
355 360 365	
cgt tcc att gct gta tgg gat atg gcc tcc cca act gac att acc ctc	1215
Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu	
370 375 380	
cgg agg gtg ctg gtc gga cac cga gct gct gtc aat gtt gta gac ttt	1263
Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe	
385 390 395	
gat gac aag tac att gtt tct gca tct ggg gat aga act ata aag gta	1311

Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val
 400 405 410
 tgg aac aca agt act tgt gaa ttt gta agg acc tta aat gga cac aaa 1359
 Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys
 415 420 425 430
 cga ggc att gcc tgt ttg cag tac agg gac agg ctg gta gtg agt ggc 1407
 Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly
 435 440 445
 tca tct gac aac act atc aga tta tgg gac ata gaa tgt ggt gca tgt 1455
 Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys
 450 455 460
 tta cga gtg tta gaa ggc cat gag gaa ttg gtg cgt tgt att cga ttt 1503
 Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe
 465 470 475
 gat aac aag agg ata gtc agt ggg gcc tat gat gga aaa att aaa gtg 1551
 Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val
 480 485 490
 tgg gat ctt gtg gct gct ttg gac ccc cgt gct cct gca ggg aca ctc 1599
 Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu
 495 500 505 510
 tgt cta cgg acc ctt gtg gag cat ttc gga aga gtt ttt cga cta cag 1647
 Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln
 515 520 525
 ttt gat gaa ttc cag att gtc agt agt tca cat gat gac aca atc ctc 1695
 Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu
 530 535 540
 atc tgg gac ttc cta aat gat cca gct gcc caa gct gaa ccc ccc cgt 1743
 Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg
 545 550 555
 tcc cct tct cga aca tac acc tac atc tcc aga taaataacca tacactgacc 1796
 Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
 560 565
 tcataacttgc ccaggaccca ttaaagttgc ggtatttaac gtatctgcca ataccaggat 1856
 gagcaacaac agtaacaatc aaactactgc ccagtttccc tggactagcc gaggagcagg 1916
 gctttgagac tcctgttgagg acacagttgg tctgcagtcg gccaggacg gtctactcag 1976
 cacaactgac tgcttcagtg ctgctatcag aagatgtctt ctatcaattg tgaatgattg 2036
 gaacttttaa acctcccctc ctctcctcct ttcaccttg cacctagttt tttcccattg 2096
 gttccagaca aaggtgactt ataaatatat ttagtgtttt gccagaaaaa aaaaa 2151
 <210> 2
 <211> 569
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence : cDNA
 coding for human beta-TrCP protein
 <400> 2
 Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met
 1 5 10 15
 Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
 20 25 30
 Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
 35 40 45

Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
 50 55 60
 Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
 65 70 75 80
 Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
 85 90 95
 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
 100 105 110
 Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
 115 120 125
 His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
 130 135 140
 Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
 145 150 155 160
 Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
 165 170 175
 Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
 180 185 190
 Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
 195 200 205
 Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
 210 215 220
 Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
 225 230 235 240
 Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
 245 250 255
 Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
 260 265 270
 Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
 275 280 285
 Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr
 290 295 300
 Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile
 305 310 315 320
 Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr
 325 330 335
 Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
 340 345 350
 Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser
 355 360 365
 Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg
 370 375 380
 Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp
 385 390 395 400
 Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
 405 410 415
 Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly
 420 425 430

Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser
 435 440 445
 Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg
 450 455 460
 Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
 465 470 475 480
 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
 485 490 495
 Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu
 500 505 510
 Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp
 515 520 525
 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
 530 535 540
 Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro
 545 550 555 560
 Ser Arg Thr Tyr Tyr Ile Ser Arg
 565

<210> 3
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence : sense primer

<400> 3
 ccaaactgcg tataacgcg

19

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence : antisense primer

<400> 4
 ggtgaatcaa cgtgtttagc

20

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence : sense primer

<400> 5
 ggatgatgta tataactatc

20

<210> 6
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence : antisense primer

<400> 6

tttatcccag atcttgattg tgttg

25

<210> 7

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence : primer

<400> 7

ccaggatcct tataacaacat tgacagcagc

30

<210> 8

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence : primer

<400> 8

ccaggatcct tagtcccaga tgaggattg

29